


```

QY 259 NKGQNTLSGLVPTKRPTEGDDPMPPNQPOTS---LIRKVAIGBYSLELGATLOLT 315
Db 761 N--QYTRELA-VPGYSQEKIDDTTKNTQKQFPLDLKATKNSSGE--KNLVGAFFELS 815
QY 316 GDVYNSEQARVFSND---IGERIELSDG-TYTLTELSNPAGYSIAEPITTFVEVA--G 367
Db 816 GKNV---QTLTVLBKMDKQSYSLPKDVRLOKGERYTLTEVKAPEGHELGKKTWTQIEVSEGG 872
QY 368 KYVTIIDKQOIEPNKQIVPEYSVEANDFEFSV---LTTQ-----NKAFTYA---K 415
Db 873 KV--SIDGEVETTTNOYV--PLEIE--NKFSSLPIRIKYTMONGKOVNLAETAFALOR 926
QY 416 NKNKSOVVCYCFNADLKSPDSEGGKTMTPDPTTGEVKYTHIAGNDLFKYVKKPDDTB 475
Db 927 NAGSYTVATQKTD-----TTG----- 944
QY 476 DTEPLHKIKYIEKG-VREKGOATEYSGLTETLOAAOTAIYVTFDSEALDKDKLDYHG 534
Db 945 ---LSYE-KISEPEYR-----AVEGSG---PLGYDILAENYEFT---VDK----- 980
QY 535 FGDMDNSTLVAKLIVYAO---DSNPQLTDLDFLIPNNKQSLIGTOWHPEDLVDI 591
Db 981 YGR-----IHYACKNIEENAPEWT----- 999
QY 592 RMEKKKEVIVPTHNLTRK---TYTGLAGDRTKDFHELEKNNKQELISQYTKDTNLT 648
Db 1000 -----LTHONNLKPRDLVYHKKADNOT-----PLKAKKRLTG---EDTD 103
QY 649 EF-KDGKAT-----INIKGE-SLTTLQGLDEGYSYLKETD---SEGYKYVNSQEVANA 698
Db 1038 ELPPDKKETDTFEVENLPGKVVLTETFTPEGQGLKEPIELIIRREGSVTIDGEVADV 109
QY 699 TVS---KTGTSOETLAFENKKEPVYPTGDOKINGLALI---VIAGISLGI 745
Db 1098 LISEKKNQITLDVT---NOAKVPLPETGIGRLWFLAISTFVIAGVYLF 1147

RESULT 2
US-09-107-532-4518
Sequence 4518, Application US/09107532
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING T
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7308
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
City: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER:
OPERATING SYSTEM:
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085598
FILING DATE: May 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Artiuello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (781)693-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4518:
SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...728
OS-09-107-532-4518

Query Match	4.68;	Score 181;	DB 15;	Length 728;
Best Local Similarity	20.7%;	Pred. No. 4.7e-06;		
Matches 147;	Conservative 102;	Mismatches 235;	Indels 226;	Gaps 37;

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QY 96 VNLGSG--RSQVYCNFKRAFPJGSSSVKWKWKHKGJSTKREDD-----A 141H
D 175 ISIGNTIKSNQIT-----LGRQOEIOIHQVPR--IOTENEDHHPNFIOMNERT 223H
QY 142 MSPRITGDELNOKLRAVYNGHPONANGIMEGLPELNAIRVTOEAVVYSDMAEISNPD 201H
D 224 FQPNIDTNEELAE-----FGPSAKAPAGVSLHT--KTLWEEEDPNLADRPDQ 267H
QY 202 -SFKRESESNIVTSQSLSMNOALKOLIDPLNAF-----KMPKQVPDDQ--LSI 247H
D 268 VTFEIQRB---HTTNAAMNGYIRIKRPAKDTTMTWERAIDKLSAHSGESYOETLSL 323H
QY 249 FESBDKGKYNKGNONLISGLVPTKPRPTQ-----DPPAPNPOQTTSY---LIRKYA 289H
D 324 POWNOGAES--YQTI-----KELPVPREYDSQIDAMTKTKTKQFTPLNKLITYNSS 374H
QY 300 IGDYSKLECATIOLITGCDNWNFSQA-WFESSNDIGERIEL-SDTYVYLTELNSPAGSIA 357H
D 375 TGE--KDLIGAVFRLTQDSIDTLTLTBGDGYSLPENVKLOKEMTYTLTLTKFAPEGHGLS 432H
QY 358 EPITFKVAGKVVYTI-IDGR-----QIENPKKEIPEYSVDAVYDFFEEESVLT 405H
D 433 KTTWEIKIASDGTVTIDGKTVTTSDDTLOLTLENPEVEV--PVAVRKRYAMQGTDKIEL 480H
QY 406 QNVAKFYYAKKKNSSSQVYVCFNADLKSPPDSE---DQGTMTPTDFTTGKYYKTHINGRD 466H
D 491 KGAAFSLQKKEANQTYO-----PDSQTTNKRGLASFDSLPGKRVAVETAGPA 539H
QY 463 LEKATVPRDDPTPLKHKIKVIEKGYREKGAIEFSGLETQRLAATOLAIYFPTDSA 522H
D 540 GY-----DTSPENYEFQIDKY-----GKIT-YTGKNTENTNWNVTLTLHONRLKAF 583H
QY 523 ELDRDKLEKDYHGFGDMNDSTLAVAKILVEYAODSNPOLDLDLFFIRNNKYOSLIGTOW 582H
D 584 DLYTHKKED-----NGQTLKGAKKFRLQ-----GPEM-DLE----- 612H
QY 583 HPEDLVDLIRMEKDEKVIAPVTHNLTLLKRYTGLAGDRTKDFHEIETLKNKQELLSTQVK 642H
D 613 SPKD-----GQETDITFLE----- 626H
QY 643 TDKTNLEFKCKQKATINLKHGE-SLTLQGLREGYSYL---VKENDSEKVKVYNSQEVANA 698H
D 627 -----NKPGRYTLTETTFTEGEGOGKLEPATTYIHEGSGSIQVQDQD--HE 668H
QY 699 TVSKTGITSD--TLAFENN--KEPVVPJGVOOKINGYALALVIYAGISIGIV 746H
D 670 SVLSPGAKNNQISDITNQAQKVPRLPETGGIGRLGATY--LVGMIGCAFSIM 717H

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: GENERAL INFORMATION:
: APPLICANT: Lynn Doucette-Stamm et al
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
: TITLE OF INVENTION: FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: GTC-005
: CURRENT APPLICATION NUMBER: US/09/134,000A
: CURRENT FILING DATE: 1998-08-13
: NUMBER OF SEQ ID NOS: 6810
: SEQ ID NO 4971
: LENGTH: 1233
: TYPE: PRN
: ORGANISM: Enterococcus faecalis
: US-09-134-000-4971

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Query Match	4.3%	Score 168	DB 15	Length 1233
Best Local Similarity	21.5%	Pred. No. 0.00015		
Matches 163	Conservative 105	Mismatches 323	Indels 168	Gaps 42

OY	39	ALYTSWAGATVYGLVES---	STPNAIDSSSEKFRWGYEESVYGHPIYKOFRAHDL	95
Db	515	SLSPTVIGPKKAIQVLSVDYIEPISVNP-	LNAETNANGTDO-----	NCAYSRR 562
OY	96	--VNLEGRSRYOYCENLKAFPP---	IGSDSSVKKWYKKKHDIgstKEDYAMSBRITGD	149
Db	150	ELNOKLRAYVNGHPONANGIMEGLE----	PLNAIRYQAEVWYISDNAPISNDESEK	204
OY	616	VIFETTPITNEIOIPGFVYVPPDSLEPKOKSI	VDPIITPMSAEGLLPVDYVTT---NSK	672
OY	205	RESESNLVSTSQLSRQALOKOLIBENLATAK	PKAPKOVDPDFOLSEISESDKGDKYKQGN	264
Db	673	RGEERLTQSSKNQFLVMAANDSFDSLSTVKT	IPRAGA--DVLEFDIYVSN--DOYDSTITPQ	728
OY	265	LLSGGLVPTKPPPTGPPMP--PNOPQTTSVLI	-----RKYAIQDYSKL--LEGATLQ	313
Db	729	YMRGQVYFDKPMTPNSPGYPTITFDENTNST	YFDFGKTKRYII--EYKNANGMIDVPTLY	787
OY	314	LTC-----DNVNSFQARFSSNDIGERLELSD	GYITTELSNPAGYSIAEPITPKVAG	367
Db	788	ITGTAKERPOSNNEGSASVQV---	EALDILISAT-----QANPILKNKYT	832
OY	368	KYVT-IIDGG--OIEPNKEIPEYSEVLEYNDE	EEFSVLTQNVAKFYAKKNGSSOVV	424
Db	833	TYVTTKIDNKTHRYKAPTELTPKGTNNADLN	STV-----KQPEBDA	877
OY	425	YCFENADLKSPPOSEDGGKTMTPDPTTGE---	VKYTHIAGRDLFKYTVARPRDTPDLTKH	481
Db	878	Y-----SLEKTTNGAKVIFKDYULTENIT	IEVMTVSNAGQIYETITLIDSELTNGQSA	930
OY	482	IKKVI-----EKYREGQOALIEYSGLETQ	LRAATQALITYFD-----SHEL	524
Db	931	SKRKVTAPITLTKFSEBGDEGIYVYLATAF	YTHNVEDENOAIKVSFELIDWHTATAEF	990
OY	525	DKOKLMDYHGFQDM-NDSTLAVAKILVEYA	OSNPOL-----DLDEFIP-----	569
Db	991	TTBEKGOYSDAIMTGDYLTFRYVNPQEI	SVDE--YLGKRAIKLYKGDNOQLKILPTTI	1048
OY	570	NNNKYO-----SLIGTQMPHEDLVLDIIR	REDK-EVIPYTHMLTKRVGTGLAGRTKDF	623
Db	1049	DHSRLQKDSITVIGDGSWKPEE--NFVSAT	KDTGQDVPE-----KIIVSGV--DNTKAG	1100
OY	624	HELEELKN-NKQELLSQIYKTDKTNLEFQD	GATINLKHGSSLTQGLPEGSIYLVKFTD	682
Db	1101	VYDIIYSDEKEETETAVTKKPDOSKLE	YVND--TIIYV-GDSWK-----PE--DNEVSATD	1150
OY	683	SEGYKV-----KVNSQEVANATVSCTG	ITSETLAPENKKE 718	
Db	1151	KTGODVPEEKIDVQGTVN--VDVIG--	DYEIIVYKNGKK 1184	

US-09-071-035-404

Sequence 404, Application US/09071035

APPLICANT: Gil H. Choi
 TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
 NUMBER OF SEQUENCES: 496
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 FAX: 301-585-0050

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

```
SOFTWARE:  ASCII Text
OPERATING SYSTEM:  MSDOS VERSION 6.2
```

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION

NAME: A. Anders Broc

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PB369P2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

SEQUENCE CHARACTERISTICS:
NEORMATION FOR SEQ ID NO: 404:

LENGTH: 1416 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

9-071-035-404

erv Match

Best Local Similarity	21.1%	Pred	No	0.00073
Best Local Similarity	21.1%	Pred	No	0.00073

Matches 159: Conservative 104: Mismatches 326: Indels 166: Gaps 40:

QY	39	ALVTSAMGATVFEVLS-----STFNAINPOSSSEYMYGYESYVRGHYKOPFVADLR	95
Db	484	SLSTFVYGPKNKAIOLVSDQYIEPISVNP-LMNTLNGNTDQ-----NGAVSSR	5311
QY	96	--VNLEGSRSYQVYCFNIAKAP---LGSDDSVYKWKYKKKHGISTYKFEDYAMSPRITGD	149
Db	532	TYVSMGSKKEPIONLEIKVHPMYLSLRATKEIYFYK---LGT---DYVTFPSDGS	584
QY	150	ELNOKLAAMVNGHPQANANGMELE-----PLNAIVTQEAAMWYYSNDAPISNPDESEK	204
Db	585	VIKETPTEITNEIOPIEFENVPDSLPKDKSIPVDTIPITMSAGELAPVDVTTVTT---NSK	6411
QY	205	RESESNVSTQSLSLMEQALKOLIDPLMLKAPQVDPDDQLSTFESEDKGDYKNQYON	264
Db	642	RGSRTTQSSKNQDFLVNARNDSPSLSVRKIRIPAGA--DVLFDIIVDSN--DOVDSITPO	697
QY	265	LLSGGLVPTKPPPTGGDPPM--PMQOPTSVLI-----RKVAIGDYSKL--LEGATLO	313
Db	698	YMDGQYFDKPMFPNSGCGYPTTFDEMTNSTYTPFCGKTNRYYI--EYKNANGMIDVPTLY	756
QY	314	LFG-----DNVNSEQARVFSSNDIGERIELSDGTYTITELNSPAGYSIAEPTFEYVAG	367
Db	757	ITGTAKEPQSNNGSASVSYON---BALDILSAT-----QANPFLKNVTKT	801
QY	368	KVYV-IIDGK--QIENNKELVEYISVEALNDPEFSVLTQNTAKFYAKKNNKNGSQYV	424
Db	802	TYVTKINDKNTHRVKNPNTIELTPKGTNTMAOIDLNSTIV-----KGVEIDA	846

FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.93804
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2516 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-851-567B-47

Query Match 3.9%; Score 152; DB 12; Length 2516;
Best Local Similarity 18.3%; Pred. No. 0.011; Indels 254; Gaps 37;
Matches 148; Conservative 120; Mismatches 287;
DB 157 AMYNGHPONANGIMEGLEPLNARVTOE-AVWYSD-----NAPISNPDESFRRESE 208
884 AQLANVAPGVSAIV-GLDYLQSMKPTPYAQMENAGVLTAGLNSQANTLHAFLDESR 942
209 SNLVST---SGLSLKRAQAKQ-----LIDPNA-----TKMPKQVDDPQL----- 246
943 SALSITYYIRQVAKAAAIKSRDRLQYLLIDNQVSAIKTRIAEALA-SIDLYVNRAL 1001
247 -SFESEDDG-----DKYKGYONLSSGLVPTKPPPTGGDPMPNPOTSVLI 295
1002 ENEENANGVISROFFIDMDKYNKRTSTWAGVSQLVYTPENTIDPTMRIGOTKMDALL 1061
296 RKYA-----IGDYSKILEGATLQLTGDVNVNSFOARVF-----SSNDIG- 334
1062 QSVSOSQALADYEDAFMGLYLSFEQVANLKVISAHDNINNOGLTYFGLSETDAGEV 1121
335 -----RIELSGTYTLT-----ELNSPAG--YSTAEPTTEKVEKGYTTI-IDGQLE 379
1122 YRSVDSHFRKNDGKAFANAMSEWHKIDCPINPYKSTIRVLYK---SRLLYLMLEQKEIT 1178
380 NPKKEIVERYSEAYKDFE-----EESVLTQN-----YAKF 411
1179 KOTGNSKDDYQETDYRYELKLAHIRYDGTWMTPTFDVNNKISELKELENNRAPGLYCAG 1238
412 YYAKN-----KNGSQVYVCFNADLKSPPDSEDDGKTMP----- 446
1239 YGEGDILLVFNQOQTLDSYKNASQGLXIF-ADMAS-----KDMTPESQNVYRDN 1289
447 -----DETTGEVKTTHLAGDLEFKYIVKPRDTPD 475
1290 SYQGFDTNNVBRVNNRYAEDEIIPSSVSSKRDYGMGDYILSMVYNGDIPITINXKAASDL 1349
476 DVFLEKIKKVIETGY-----REKQALEYSGTLTQLAATQALAIYFTDSAELEDKKLD 531
1350 KIYISPKLRITIHNGYEGQRKNCNMLNKKYKGLGDKFIVTSLGVDNPNSSNKLMEFYVVO 1409

DB 532 YHGFDMNDSTLAIAKIIIVEAODSNPPOLDDEFFIPNNK-----YOSLIGTOM----- 582
1410 YSG-----NTSGINOCRL--FHRTTYP--SKVEAMIGKAKSLITNONAAIGDDYATDSL 1461
583 -HPEDLVDIRBEDKEVI-----PVTHNLTL--RKTVTGLAGRTKDFHE----- 626
1462 NKFDLKOYIFMTDSKGRATDVSGVEINTAISPAKVOIYVAGKGEQFTADKQVSTOP 1521
627 -----IELKNNKOBLLSQVTKDTNLEF-KDGK-----ATINLKHG 662
1522 SPSPDEMNQFNALEIDSGLNFINNSASIDVTFEAFEDGKRLGESFSLVPTLKVESTD 1581
663 ESLTLQGLPEGYSLVYKETEDESGYKVNVS-----QEVANATSKGIGISDELAEENKE 718
1582 NALTLEHNENGAQVM-----QWOSYRTRNLTPLEAROLVARAT--TGIDTILSMETONIOE 1634
719 PVVPTGVDDKINGVLLALYIAGISIGIMG 747
1635 P-----QLGKGFYATVYIIPPYNLSTHG 1656

RESULT 8
US-09-327-536-2
Sequence 2, Application US/09327536
GENERAL INFORMATION:
APPLICANT: FISCHETTI, Vincent A.
TITLE OF INVENTION: FIBRONECTIN AND FIBRINOGEN BINDING PROTEIN FROM GROUP A
TITLE OF INVENTION: STREPTOCOCCI
FILE REFERENCE: 022927-008
CURRENT APPLICATION NUMBER: US/09/327,536
CURRENT FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: US 08/714,402
PRIOR FILING DATE: 1996-09-16
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1161
TYPE: PRT
ORGANISM: SFFBP gene
US-09-327-536-2

Query Match 3.8%; Score 150; DB 17; Length 1161;
Best Local Similarity 19.9%; Pred. No. 0.0045;
Matches 191; Conservative 121; Mismatches 326; Indels 324; Gaps 51;
DB 21 KNSKRTYTLV--GVPLMT-----FALVTSWVGAKTVFGLVESTPAIINPDSSSEYRW-- 72
112 KTSRTVTVTVYENGTYKTLVBNPYNGELISKAGSKDV-----SSLDLENPKKSYVSKYK 166
73 ---YGESYVRGHPY-----KQ-----FRVAHDLRVNLEGSRSYOVYCF 109
167 TEYSSGAAPFYRNHAAVYFKMSFELKQDKSEITINPDGTVLQDRRLNKG----- 217
110 NUKKAP-----LGSDDSVKWKYKHDGISTKFEDYA----- 141
218 -ISQDIPKIIYDSANGPLAIGKYAHENHOLIYFTFTYIAGLDKVOLSABLSIFLENKEVL 276
142 -----MSPRITGDELNOK--LRAVMYNGHPONANGIMEGL-----EPLNARVTOE 185
277 EMTSISNFKSTIGGQELITTKGTAVNLVYGNESYKESNYITNGLSNNGSIESYVT--ETGE 334
186 AWYYSQDNAPISN-PDESFR-----RESESNLVSTQSLSLKRAQALQOLIDPNLATKMP 237
335 FWWYVYVNPRTNIPYATAMLMGFGARASNTSDLENDANTSSAELEIYVYEVPEGEKLP 394
238 KOVPDD-----FOLSESEDDGDK-YNKGY----- 262
395 SSVGVADVTKLTLTDTIAGLNGFQMTKRORIDFNKNKAFIIVTKTDOGSKPLV 454
263 -QNLLS-----GG-----LVPTKPTTGDDPMPNPNOQTSTVILRKXA 299

Db 455 QSNLASRGAEEAFTPGVGNVYFQNETALSPSKSGSGKSEF---TKPSITVANKRVA 512
Qy 300 IGDYSL-----LEGATIQLTGDNVNSFOARVSSNDIGE--RIELSDGTYLTELNSP 331
Db 513 QLFKMSIDNVPLPEAAELRSSNGNS--QKLEASNTGQEVHFKDLTSGTYDLTEFKAP 571
Qy 352 AGYS-----IAEPIF-----KVEAGVYTIIDGKO--IENPKNIVE 387
Db 572 KGIQOQTEKLAITYVDTTPRAEBMTWGSBPHSSVKEANEVITVNHKEITLTFSGKKIME 631
Qy 388 PYSVEAYNDFEERSVLTTONYAKFYAKKNKSSQVYCFNADLKSPSEDEGKMTPTD 447
Db 632 -----NRPD-----QRPAKIQVQLQNGO-----KMPNOQOE-----VTKD 663
Qy 448 FTTGEVYTHIAGRDLPKTYVPRDTPDTPELKHAKVIEKGYREKQALIESGLTETOL 507
Db 664 ---NDMSY--HF--KDLPRKDAKNOE-----KYSVEEVAVPQGYKYSYLGNDIFNT 708
Qy 508 RAATOLAIFYTDSAEIDMDKLDYHGFDMNDSTLAVAKILVEYADDS--NRPOLDLD 565
Db 709 R-ETEFVEFQONNENLEFGNAELKGSQSKIIDDITLTFSGKIMKNDYAEKRPQAIQVO 767
Qy 566 FE-----IPNNKYOGLIGTOMHP-----DLV-----D 589
Db 768 LVADGVAVEGQTFEISGNGNEMSEFEKNLKKYNGTGNDIISYKEVTVPTGYDVTYSAND 827
Qy 590 IIRMEDEKEVI-----PYTNHLTKTYVTLGAGRTYDFHEIE---LKNKKOELL 638
Db 828 II--NNKREVITQOQPKLEETLPLESGASG--GTTVEDSRPVDLTLSGSEQCSGD 883
Qy 639 QVKTOK--TNLEK-----DOK-----ATINLKHESLTLG-----LPEGYSL 677
Db 884 MTEEDSATHIKSKDKDCKELAGATMELROSSGKTIISTWISDGOVDYLPKGTTF-- 942
Qy 678 VKETDEGKYV-----KNSQEVANATVSKGTISDETLAFENKEPVVPTG-----VDQ 727
Db 943 VERAAPDGEIAIAITFTYNEO--GOVTYNGKATKGDTHVMDAKKPTGSGQVIDIE 1000
Qy 728 KI 729
Db 1001 KL 1002

RESULT 9
US-09-200-650-5
; Sequence 5, Application US/09200650
; GENERAL INFORMATION:
; APPLICANT: Foster, Timothy J.
; APPLICANT: Eidlun, Delordre N.
; APPLICANT: Hook, Magnus A.O.
; APPLICANT: Perkins, Samuel L.
; TITLE OF INVENTION: Fibrinogen-Binding Proteins from Staphylococcus aureus
; FILE REFERENCE: 09910-0100P
; CURRENT APPLICATION NUMBER: US/09/200,650
; CURRENT FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: 60/066,815
; EARLIER FILING DATE: 1997-11-26
; EARLIER APPLICATION NUMBER: 60/098,427
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1315
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-200-650-5

Query Match 3.8%; Score 149; DB 16; Length 1315;
Best Local Similarity 20.2%; Pred. No. 0.0068;
Matches 203; Conservative 93; Mismatches 336; Indels 372; Gaps 45;

Qy 8 NKINTINTQVLSKNS--KRFYTVLVGVFLMIALVTSNMGATVAGLVESSTP----- 59

Db 208 NSNNENNADIIILPKSTAPKRLNTR-----MRIAAPSSSEAKANNVDLITSNTTLVVDA 262
Qy 60 ---NAINP--DSSSEXYRWYGESYVGHPPYKQFRAHADLRNMLEGSRYSQVYCFNLKRA 114
Db 263 DKNNKIYPADYLSLKSQTLVDKKSQDYF-----TIKSDYQVYGLMPEDI 311
Qy 115 FPLGS-----DSSVKKYKHKHDG-----ISTKFEDYAMSPTIGELQKLAAYVNGH-- 163
Db 312 KNIGIDKPNNGEITATKADIDANNLITFTDYV-----DRFNSVOMGIVYSIYMDA 364
Qy 164 ---PONANGIMEGLEPLNALIRVQEAVMYSDNAPISNPDESFKRESNUL----- 211
Db 365 DTIPVSKNDYEFNVTIGNTTKTTANIQYDPDYVNEKNSIGSAFTEVSHVKGKENPGY 424
Qy 212 ---VTSQSLMRQALK---QLIDPNLATMPKPOVPDOLFSESEKDGKYNKY 262
Db 425 KQTIYVNPSENSLTNKAKLKQAVHSSYPNNIGQINKDVTD---IKIYQ--VPKGYTLNKGY 480
Qy 263 QNLSGGLVPTKPTPGDDPPMPNPOTTSVLIRKTAIGYSK----- 305
Db 481 D-----VTKELT-----DVTNQLKITYGDNNSAVIDFGNADSAVYVMVN 522
Qy 306 -----LLEGATIQLTGD-----NY 319
Db 523 TKFOYTNSESPILVQAMATLSTGKNSYSTGNALGFTNNQSGAGQVYKIGNTVWEDTNK 582
Qy 320 NSFQ-----ARFESSN--DIERIELSDGTYYLTLE-----NSPAGYS 355
Db 583 NGVQELGEKGVGNVTVYFDMNTNTRKVEAVTKEDGSYILPNLPGDGYRVEFNLPRGYE 642
Qy 356 IAE----- 358
Db 643 VTPSKQGNNEELDSNGLSVITVNGKDNLSADLGIXPKXNLGDIYVWEDTNKNGIDODE 702
Qy 359 -----PIPEKVEAGKY-----TLIDCK-----QIENPKKEI-----VEPYSVEAYNDF 397
Db 703 KGISGYTVTLKDNNGVNLKIVTTDADGKRYFTDLNNGNRYVEETTPGTYPTVTSQSDI 762
Qy 398 EEPF-VLTTONY-----AKFYAKKNKSSQVYCFNADLKSPDSED--GKRT 443
Db 763 EKDSNGLTTGVINGADNMWTLDSGFYKTPKYNLGNVYWEDTNKDGKO--DSTFKGISGYT 820
Qy 444 MTPDFTTGEVYTHIAGRD--LEKTYVPRDTPDTPELKHAKVIEKGYRKGGAIEF--- 499
Db 821 VTLKNEGEVLTQTKDKOKGYOFT-----GLENGIYKVEFERP 859
Qy 500 SGLTEPQLRAATQALAI--YYTDSAEIDKOK-----LKDY-----HGFG 536
Db 860 SGITPTQVSGSDEIDGIDSGNSTGTCYAKDKDNDTIDSGFYKPTPNLGDYVWEDTNKNGVO 919
Qy 537 DMDNSTLAVA-----KIIVEYADSNP--QLTDLDFEPIPNKKYOSLIGTOMHPED 586
Db 920 DKREKISGTVTLKDNCKDVKLTVTVDENGKRYQFDL-----NNGYK-- 963
Qy 587 LVDIIRMEDEKEVIP--VTHNLTLRK-----YVTGL---AGRTKQPHFEIELKNNKQEL 636
Db 964 ---VEFERPSSGYTPTSVTSVSGNDEKDSNGLTGTGYIKDNDNTLDSGF---KTKPKYSYL 1016
Qy 637 -----LSQTVTKDTKTNLEFKDKGKATINKHGESLTLGSLPBGYVLYVETDEGKYK 689
Db 1017 GDYVWYDSNKGDKODSTENGKIKDYKVTLLNEKGEVIGTTKTEDNGKCYCPDNLDGKRYKI 1076
Qy 690 VNSQEVANATVSKGTISDETLAFENKKEPVVPTGVYDOKI--NGY 732
Db 1077 F--EKPRAGLTGTGTNTTEDDKADGGEVDVITIDHDFTLIDNGY 1118

RESULT 10
US-09-200-650A-5
; Sequence 5, Application US/09200650A
; GENERAL INFORMATION:
; APPLICANT: Foster, Timothy J.

APPLICANT: Edhinn, Deirdre N.
APPLICANT: Hook, Magnus A.O.
APPLICANT: Perkins, Samuel L.
TITLE OF INVENTION: Fibrinogen-Binding Proteins from
TITLE OF INVENTION: Staphylococcus aureus
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Akeve, LLP
STREET: 191 Peachtree Street, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/200,650A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/066,815
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Jamie L.
REGISTRATION NUMBER: 32467
REFERENCE/DOCKET NUMBER: 09910-0100P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 4048183700
TELEFAX: 4048183799
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1315 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
AMT-SENSE: NO
FRAGMENT TYPE: N-terminal
US-09-200-650A-5

Query Match 3 8%; Score 149; DB 16; Length 1315;
Best Local Similarity 20.2%; Pred. No. 0.0068;
Matches 203; Conservative 93; Mismatches 336; Indels 372; Gaps 45;
DB 8 NKLINTNORVLSKNS--KRFVTLVGVPLMIPALVTSWVGAKTVEGLVESSTP----- 59
DB 208 NSNENENNADIIIPKSTAPKRLNR-----MRIAAYQPSSTEAANNVDLITSNTTLVYDA 262
QY 60 ---NAINP--DSSEYRWYGYESYVRGHYYKQFRVAHDIRVLEGRSRYQYVCENIKKA 114
DB 263 DKNKKIVPAQDYLSLRSQITLVDDKVKSGVF-----TIKYSDFVQVYGLPEDI 311
QY 115 FPLGS---DSVKKMYKKKHDG---ISTFEEDYAMSPRTGDELNOKLAAVYNGH--- 163
DB 312 KNIGIDIKDPNNGETITAKHDITANNLITTYFTTYV-----DRENSVOMGINTYIYMA 364
QY 164 ---PONANGIMEGLPELNAIRYQEAUVWYSDNAPISNPDEFKRSSESNL----- 211
DB 365 DTFVSKNDVEFVNTIGNTTKTANIOYPDYVNNKNSIGSAFTEVSHVGNKENGY 424
QY 212 ---VSTQSLIMKALK---QLIDPNLATMPKOVDPDFOLSTFESDKDKDKYKGY 262
DB 425 KOTIVVNSSENSILNKKIKQVAYHSSYPNIGQINKDVTD---IKIYQ--VPKGYTLNKG 480
QY 263 QNLSGLVPTKPTPGDPPMPNPNQOTSVLIRKXVAGIDYSK----- 305
DB 481 D-----VNTKELT-----DVTNQYLOKITTYGNNNSAVIDFGNADSAVYVNVN 522

QY 306 -----LLEGATLQLTGD-----NV 319
DB 523 TKFOYTNSEPTLYOMATLSSKNSVSTGNALGFTNNOSGAGQEVYKIGNYWMETNK 582
QY 320 NSFQ-----ARVSSN---DIGERIELSDGTITLTL-----NSPAGS 355
DB 583 NGVOELGKGVGNVYVYEDNNTNTRKVGAVTKEDGSYILPLPNGDYRVERPSNLPKGE 642
QY 356 IAE----- 358
DB 643 VTPSKOGNNEELDSNLSSVITVNGKDNLSADLGITKPKYNLDGVWEDTNKNGIQDDE 702
QY 359 -----PITFKVAGKY---TIIDK---QIENPKKEI-----VEPTSEAYNDF 397
DB 703 KGISGVYTLKDENGNVLKTYTDDADGKYKFTDLDNGNKYVEFTPEPTPTVYSGSDI 762
QY 398 EEFS-VLTQNT-----AKFYAANKNGSSQYVYCFNADLKSPDSBD---GKKT 443
DB 763 EKDSNGLTTTGVINGADNNTLDSGFYKTPKYNLDGVWEDTNKDKQ--DSTKGISGV 820
QY 444 MPDFTTGEVKTTHIAGRDLFKYTVKPRDTPDFLKHKKVIEKGYREKQALTEY--- 499
DB 821 VILKNGEVLDTTKDKDKQKQFT-----GLENGYKVEFETP 859
QY 500 SGLTETQLRAATQALAYFTDSAEIDDK-----LKY-----HGRG 536
DB 860 SGYPTQVSGTDEGIDNSGTSTGVYIKDKNDJIDSGFYKPTYNLDGVWEDTNKNGY 919
QY 537 DANDSTLAVA-----KIIVYAKDSNPP-QLTDDLFFIPNNKKYOSLGTQWHPED 586
DB 920 DKDEKISGVYTLKDENDKVLKTYTDDNGKYQFTDL-----NNGTYK----- 963
QY 587 LVDIIMEDEKKEVIR--VTHNLIRK-----TVTGL---AGDRTKDFHEIELKNNKQEL 636
DB 964 ----VEFTPSGTYTPSVSGNDTEKDSNGLTTTGVIKADNMTLDSG---YKTPKYSL 1016
QY 637 -----LSQVYTKTNLEPKDGKATNLKHGESITLQLEPGSYLYLKEPDSSEYK 689
DB 1017 GDVWYDSNKKDGKODSTEGIRKDVKTYTLNKEGEVIGTKTDENGKYCPDNIDSGKYKI 1076
QY 690 VNSQEVANATVSKTGTSDETLAFENKKEPVYPTGVOKI-NGY 732
DB 1077 F-EKPAGLTGTGTNTEDDKADGGEVDVTTIDHDFTLDNGY 1118

RESULT 11
US-09-071-035-458
Sequence 458, Application US/09071035
GENERAL INFORMATION:
APPLICANT: Gail H. Choi
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 496
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes

REGISTRATION NUMBER: 36,373
 REFERENCE/DOCKET NUMBER: PB369P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 458:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2032 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-071-035-458

Query Match 3.8%; Score 149; DB 14; Length 2032;
 Best Local Similarity 19.0%; Pred. No. 0.014;
 Matches 178; Conservative 117; Mismatches 330; Indels 310; Gaps 44;

QY 19 LSKNSKRFYTLVGVFLMIFALVTSWY-----GAKTVFG-----LVESSTPNAI 62
 DB 1098 LKRTADETTILAGAHQIWDQAKTVLRGTYDAGVITFFGGLPGQYILVETKAP--- 1154
 QY 63 NPDSSSEYRWYGYESYRGHPYKQFRVAHDLRVNLEGSRSYQYCCFNLKAPPLGSDSS 122
 DB 1155 -----EGTVSDELAKGRVITIDEETSAEGAOP--TIKNDVKNVLEKKDEK 1200
 QY 123 VKRW---YKHDGISTKF---EDYAMSPRITGDELNOKLRAYVNGHPONANGIME--G 173
 DB 1201 GKRLVNAKFLKLEHAIVTPTFHMEVPLAPDRT-----NANGQLEVDS 1242
 QY 174 LEP-LNAIRYTOEAWWYYSNAP-----ISNPDSFRRESN 210
 DB 1243 LKPGVLQFTIEAPRTGLDTPTRKRFIVTQNTSGQIRDVHVKNLNYOGSAELIKKQDAGN 1302
 QY 211 LVSTQSLSLM---RQALQK--LIDPNLATKMPKQVPDDPOLSTFESBDKDKYKNGYQNL 265
 DB 1303 PLAGAESVLDITGQAVREHLVSDANKVYVTDLAPGKYOP---VETKAP----- 1349
 QY 266 LSGGLVPTKPTTPGDDPPMPNPOT-----TSVLIRKAYIGDYSKLLEGATIQ 313
 DB 1350 -AGVLLNTEPSAFTIAASDRGKPAVATATANFVNYGTAIKKIDVNG---HLLSGATFK 1405
 QY 314 LTGDNNNSPARFSSNDIGERT--ELSDGTYYLTLELNSAGYSI--AEPTTFKY---EAG 367
 DB 1406 VLDAGGETIQTGL--TTNMOGEIYAEHLAPKRYREVEFKAPGTGLANTTTPVPFELAEKNAG 1464
 QY 368 K-----VYTIIDCKOIEPNKKEIYEPYSVAYNDPEEFSVLTQNTAK-- 410
 DB 1465 KPAVVVNASDNFVSKGAFQIVKTNNSADQPLAGAV---FELY--DHNKQSLGITATSGKDG 1519
 QY 411 -----FYVANKK-----NGSSQVVC-----FNADLKSPDSDGCKMTPTDF 448
 DB 1520 KIIFRLDLPAGTYYYKEIKAPKLDPGADYIIYPELVKVEIRGDKGDEI-----F 1569
 QY 449 TTEEVKTYTHIAGADLKRKYTKPRDTPDTFLKHKIKYIEGCR-----EKGQAL--- 497
 DB 1570 QLDG--AFANKGRAVFERKKIDANANPLPGTIFKLYR--IENGKEIFEREVYAEKDGSLAME 1625
 QY 498 -----EYSGLDRETOLRAATOLATYYF-----TDSAEILDKDKLDKHG--FG--DMND 540
 DB 1626 DLGAGSELDDELATDGYLYNKQPIFYVKKNSNDKQPLDELEFVNYQAQVYMGKRVNEOG 1685
 QY 541 STLAVAKIIVEYADNSNPQTLDDLDFEIPNNNKYQS----- 576
 DB 1686 QTLGAVFAIYNDDEQNGPSPITFLNRAGEKYSSEITTDKGTETIYAKGLNEGYVLVET 1745
 QY 577 -----LIGQMPREDLVLDIIRMEDKKEVYIPVHNLTLEKTYVGLAGDRKDKHFELEK 630
 DB 1746 KAPGTYLDTTLHP---FDVTAQLGKEQPIALDLDLNYQSTA-----QLTKE 1789
 QY 631 NNRQELLSTGV--KTDKTNLEFKDGKATI--NLKHGESLTLQGLPEGY-----SYLV 678
 DB 1243 LKPGVLQFTIEAPRTGLDTPTRKRFIVTQNTSGQIRDVHVKNLNYOGSAELIKKQDAGN 1302

DB 1790 NETGEALAGAVFKVIDETG-QTVDGQTNLMSKDGKVIANKLAPGTYREVTQAPTSTYL 1848
 QY 679 KEIDSEGYK-----YKVSQEVYANA----- 638
 DB 1849 NEPPSASFITIAKNQGNKPAVVLKAPINYGAKLVKIDQKNALAGAEFKYTDAGTQ 1908
 QY 699 TVSKTGITSDETLAFENKKEPVVPTGVDOKI--NGY 732
 DB 1909 TVAKSLRSDNQGVLQVNNHLPQGKTFVEYETKAPDGY 1943

RESULT 12
 US-09-071-035-462

; Sequence 462, Application US/09071035

; GENERAL INFORMATION:

; APPLICANT: Gil H. Choi

; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

; NUMBER OF SEQUENCES: 496

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; FILING DATE: US/09/071, 035

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: A. Anders Brookes

; REGISTRATION NUMBER: 36,373

; REFERENCE/DOCKET NUMBER: PB369P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 309-8504

; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 462:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2032 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-071-035-462

Query Match 3.8%; Score 149; DB 14; Length 2032;

Best Local Similarity 19.0%; Pred. No. 0.014; Mismatches 330; Indels 310; Gaps 44;

QY 19 LSKNSKRFYTLVGVFLMIFALVTSWY-----GAKTVFG-----LVESSTPNAI 62
 DB 1098 LKRTADETTILAGAHQIWDQAKTVLRGTYDAGVITFFGGLPGQYILVETKAP--- 1154
 QY 63 NPDSSSEYRWYGYESYRGHPYKQFRVAHDLRVNLEGSRSYQYCCFNLKAPPLGSDSS 122
 DB 1155 -----EGTVSDELAKGRVITIDEETSAEGAOP--TIKNDVKNVLEKKDEK 1200
 QY 123 VKRW---YKHDGISTKF---EDYAMSPRITGDELNOKLRAYVNGHPONANGIME--G 173
 DB 1201 GKRLVNAKFLKLEHAIVTPTFHMEVPLAPDRT-----NANGQLEVDS 1242
 QY 174 LEP-LNAIRYTOEAWWYYSNAP-----ISNPDSFRRESN 210
 DB 1243 LKPGVLQFTIEAPRTGLDTPTRKRFIVTQNTSGQIRDVHVKNLNYOGSAELIKKQDAGN 1302

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OY 211 LVSTQSLSM---RQALKQ--LIDPNLATKMPKQVPPDDFOLSTIFESDCKGDKYKNGYQNL 265
DB 1303 PLAGAEFSVLDITGQAVREHLVSDANGKVTYVTLAPGKYOF---VETKAP----- 1349
OY 266 LSGGLVPTKPTGPDPPMPNPOT-----TSVLIRKVAIGDYSKLEGGATLQ 313
DB 1350 -AGYLTNTPSAFTIAASDNGKPAVYATANFVNYGSTATLKKDVG---HLLSGATFK 1405
OY 314 LTGDVNSFQARVSSNDIGERI--ELSDGTYLTELNSPAGYSI-AEPTTFKV---EAG 367
DB 1406 VLDKGETIOTGL-TTNNGEIVAEHLAPGKYRFEVETKAPTGYLNTTVPVFEIAEKRNAG 1464
OY 368 K-----VYTIIDGKQIENPKKEIYEPVSAVYNDFEESVLTQNTAK-- 410
DB 1465 KPAVVASDNFVSKGAFQIVKTNADQPLAGAV---FELY-DHNKOSGIGITATSGKDG 1519
OY 411 -----FYAKNK-----NGSSQVYC-----FNADLKSPPDSGDKTMTPDF 448
DB 1520 KIIFRLAPGTYIYKKEIKAPKLPGADYIIPELVKVEIRGDFGDEI-----F 1569
OY 449 TTGEVKTTHAGRDLEFYTKPRDTPDFLKHKKIYIEKGR-----EKGQAI--- 497
DB 1570 QLG--AFANKRGAFFKKIDANANPLPGTIFKLYR--IENGKEIFEREVYAEKDGSIAME 1625
OY 498 -----EYSGLETQLRATOLAIYF-----TDSAEIDKDKLDYHG--FG--DMND 540
DB 1626 DLGAGSELDLDTAGIYNNKOPITFYVVKNSNDKOPDLELEFVYQAEVMGRKYNQEG 1685
OY 541 STLAVAKILVEYADSNPQJTDLDFEIPNNKXOS----- 576
DB 1686 QTLAGAFALYNDQONPGSPITFELNRAGEKVEITTDKGTGEIYAKGNEGHVYLVET 1745
OY 577 -----LIGQWHPEDLVDIIRMEDKKEVLPVTHNLTKRTVYGLADRRKDFHEIELEK 630
DB 1746 KAPTYLDTTLHP---FDVTAQIGKEQPIALGDLINYGTA-----QLTKE 1789
OY 631 NNRQELISQTV--KTDTNLEFKDGKATI-NLKHGESLTQGLPEGY-----SYLV 678
DB 1790 NENGELAGAVFYIDBTG-QYVDGQTNLMSDQNGKVIANKIARFYETQAPSTYLL 1848
OY 679 KETDSEGYK-----VKVNSQEVANA----- 698
DB 1849 NEPPASFTIAKDNQGRPATVVLKAPINYGAAKIVKIDQKRNALAGAEKVTDAETQ 1908
OY 699 TVSKTGITSETLAFENKKEPVVPTGVOKI-NGY 732
DB 1909 TVARSLRSDNOGLVQVNHLPGRKYTFVETRAPDGY 1943

RESULT 13
US-09-071-035-466
; Sequence 466, Application US/09071035
; GENERAL INFORMATION:
; APPLICANT: GIL H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/071,035
; CLASSIFICATION:

```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 466:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2032 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-071-035-466

Query Match 3.88; Score 149; DB 14; Length 2032;
Best Local Similarity 19.08; Pred. No. 0.014;
Matches 178; Conservative 117; Mismatches 330; Indels 310; Gaps 44;

OY 19 LSKRSKFFTVTLGVFLMIFALVTSNV-----GAKTVFG-----LVESSTPNAI 62
DB 1098 LKRTAMEETIILAGAHQIMDOAKTQVLRGTYDAGVITIFGGLPGQOQIIVETKAP--- 1154
OY 63 NPDSSSEFYMYGYESVYGRHPYTKQFRVAHDLRVNLEGSRSYOVYCNLKAAPPLGSDSS 122
DB 1155 -----EGYVSDELAKGAVITIDEETSAEAGAP-TLIKNDVKNVLEKKDER 1200
OY 123 VKRW---YKHDGISRKF---EDYAMSPRITGDDELNQKLRAVYNGHPQANGIME--G 173
DB 1201 GKILVNARFLEHNAVTPPTFHWEVPLAPDT-----NANGOLEVDS 1242
OY 174 LEP-LNAIRYTOEAWVYYSNAP-----ISNPDESFRSESEN 210
DB 1243 LKGLVGYFTLEIAPVGLDITTPKRFIVTQTSQIRDVHVKMLNYGSAELLKKQDAGN 1302
OY 211 LVSTQSLSM---RQALKQ--LIDPNLATKMPKQVPPDDFOLSTIFESDCKGDKYKNGYQNL 265
DB 1303 PLAGAEFSVLDITGQAVREHLVSDANGKVTYVTLAPGKYOF---VETKAP----- 1349
OY 266 LSGGLVPTKPTGPDPPMPNPOT-----TSVLIRKVAIGDYSKLEGGATLQ 313
DB 1350 -AGYLTNTPSAFTIAASDNGKPAVYATANFVNYGSTATLKKDVG---HLLSGATFK 1405
OY 314 LTGDVNSFQARVSSNDIGERI--ELSDGTYLTELNSPAGYSI-AEPTTFKV---EAG 367
DB 1406 VLDKGETIOTGL-TTNNGEIVAEHLAPGKYRFEVETKAPTGYLNTTVPVFEIAEKRNAG 1464
OY 368 K-----VYTIIDGKQIENPKKEIYEPVSAVYNDFEESVLTQNTAK-- 410
DB 1465 KPAVVASDNFVSKGAFQIVKTNADQPLAGAV---FELY-DHNKOSGIGITATSGKDG 1519
OY 411 -----FYAKNK-----NGSSQVYC-----FNADLKSPPDSGDKTMTPDF 448
DB 1520 KIIFRLAPGTYIYKKEIKAPKLPGADYIIPELVKVEIRGDFGDEI-----F 1569
OY 449 TTGEVKTTHAGRDLEFYTKPRDTPDFLKHKKIYIEKGR-----EKGQAI--- 497
DB 1570 QLG--AFANKRGAFFKKIDANANPLPGTIFKLYR--IENGKEIFEREVYAEKDGSIAME 1625
OY 498 -----EYSGLETQLRATOLAIYF-----TDSAEIDKDKLDYHG--FG--DMND 540
DB 1626 DLGAGSELDLDTAGIYNNKOPITFYVVKNSNDKOPDLELEFVYQAEVMGRKYNQEG 1685
OY 541 STLAVAKILVEYADSNPQJTDLDFEIPNNKXOS----- 576
DB 1686 QTLAGAFALYNDQONPGSPITFELNRAGEKVEITTDKGTGEIYAKGNEGHVYLVET 1745
OY 577 -----LIGQWHPEDLVDIIRMEDKKEVLPVTHNLTKRTVYGLADRRKDFHEIELEK 630

```

Db 1746 KAPGYLLDPTLHP---FDVTAOLGKEOPIALGDLINVOGTA-----QLTKE 1789
QY 631 NNKOLLISQVY--KTDTNLEFKDGKATI--NLKHGESLITLOGLEGY-----SYLV 678
Db 1790 NETGEALAGAVFKYIDETG-QTVDGQTNLMSDKOGKYIAKRLAPGYTRFVETQAPTSTYLL 1848
QY 679 KETDSEGYK-----VKVNSQEVANA-----698
Db 1849 NETPSASFTIAKDNQOGKRPATVVLKAPFINTOGAAKLKVIDQOKNALAGAEFKVTDAETGQ 1908
QY 699 TVSKTGITSETLAFENNKKEPVVPTGVDOKI--NGY 732
Db 1909 TVARSLSRSDNOGLVQVNHLOPGKYTFVETKAPDGY 1943
RESULT 14
US-09-134-000-6612
; Sequence 6612, Application US/09134000A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS
; TITLE OF INVENTION: FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-005
; CURRENT APPLICATION NUMBER: US/09/134, 000A
; NUMBER OF SEQ ID NOS: 6810
; SEQ ID NO 6612
; LENGTH: 2054
; TYPE: PR1
; ORGANISM: Enterococcus faecalis
US-09-134-000-6612

Query Match 3.8%; Score 149; DB 15; Length 2054;
Best Local Similarity 19.0%; Pred. No. 0.014;
Matches 178; Conservative 117; Mismatches 330; Indels 310; Gaps 44;

QY 19 LSKRSKRFYTLVGVFLMIFALVSMV-----GAKTYFG-----LVSESTPAI 62
Db 1120 LKKTAMDETTIILAGAHQIMQDAQTQVLRGTVDATGVTIFGGLPQOQYILVETKAP--- 1176
QY 63 NPDSSEYRWYGESEYRGHPYKQFRVAHDLRVNLGSRSEYQYCFNLKAPFLGSDSS 122
Db 1177 -----EGYVSDELAKGRVITITDETSABCAQD--TIKKDVNKVLEKXDEK 1222
QY 123 VKKM---YKHKDISTRK---EDYAMPRTITGDELNOKLRAVYNGHPONANGIME--G 173
Db 1223 GKRLVNAKRLKHAHVTPPTFMEEVPLAPDRT-----NANGQLEVDS 1264
QY 174 LEP-LNAIRYTOEAVWYYSNAP-----ISNPDESFRSEBSN 210
Db 1265 LKPLGYGTEIEAPGTGYLLTPPKRFIVTONTSGQIRDVHVKMLNYOGSALLIKKDAQGN 1324
QY 211 LVSTISOLSLM---RQALKO--LIDPNLATKMKQVPPDDFOLSTFESBKGDKYKGYQNL 265
Db 1325 PLAAEESVLDITGQAAREHLVSDANKVYVTDLAPKTYD---VETKAP----- 1371
QY 266 LSGGLVTPKPTPGDPPMPNPQOT-----TSVLIRKATGADSKLLEGATLQ 313
Db 1372 -AGVLTMTPEASFTIASSDGRKPAVTATANFVYOGTAKRIKIDVNG---HLLSGATFK 1427
QY 314 LTGNVNSFOARVSSNDIGERT--ELSDGTYYITELNSPAGYSI--AEPTFKV---EAG 367
Db 1428 VLDAKGETIQTGL--TTNNOGEIVAEHLAPGYRFEVETKAPGTGYLLNTTPVPFELAEKNAG 1486
QY 368 K-----YTTIDGKOIENPNKEIPEYSVEAYNDFEESVLTQNYAK-- 410
Db 1487 KPAVYVASDNFVSKGAFQIYKTSADQPLAGAV---FELY--DHKOSIGITITSGKDQ 1541
QY 411 -----FVYAKNK-----NGSSQVYVC-----FNADLKSPPDSEDCGKTMTPDF 448
Db 1542 KIIRDLAPGTYYYIKETKAPRLPGADYIITPBLVKEIRDDFGDPEI-----F 1591

QY 449 TTGEVKTTHIAGRDLEKRYVKPRDTPDFLKHKKIYLEKGYR-----EKGQAI--- 497
Db 1592 QLG--AFANERGRAVFEKIDANANPLPGTIFKLYR--IENSEKLFEREVTAEKDGLAME 1647
QY 498 -----EYSGLFETQOAAATQALAIYF-----TDSALDKDKIKDYHG--FG---DMND 540
Db 1648 DLGAGSYELDELDTDGYIVAKQPIYVYVKKNSNDKQPLDLELEVNVQAEVNGKRVNQG 1707
QY 541 STLAIVAKILVEYADSNPPOLTDIDFFIPINNKYO-----576
Db 1708 QTLGAVFAIYNADQNOPOGSPITFLNRAGEKVEITTDKGEIYAKGLNEGHVLEVE 1767
QY 577 -----LIGTQMHPELDVDIRMEDKKEVTPYTHNLRLKTYVGLADRDKDFHELEK 630
Db 1768 KAPGYLLDPTLHP---FDVTAOLGKEOPIALGDLINVOGTA-----QLTKE 1811
QY 631 NNKOLLISQVY--KTDTNLEFKDGKATI--NLKHGESLITLOGLEGY-----SYLV 678
Db 1812 NETGEALAGAVFKYIDETG-QTVDGQTNLMSDKOGKYIAKRLAPGYTRFVETQAPTSTYLL 1870
QY 679 KETDSEGYK-----VKVNSQEVANA-----698
Db 1871 NETPSASFTIAKDNQOGKRPATVVLKAPFINTOGAAKLKVIDQOKNALAGAEFKVTDAETGQ 1930
QY 699 TVSKTGITSETLAFENNKKEPVVPTGVDOKI--NGY 732
Db 1931 TVARSLSRSDNOGLVQVNHLOPGKYTFVETKAPDGY 1965

RESULT 15
US-60-269-308-4438
; Sequence 4438, Application US/60269308
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, RW
; APPLICANT: Ohlsen, KL
; APPLICANT: Zyskind, JW
; APPLICANT: Trawick, JD
; APPLICANT: Wall, D
; TITLE OF INVENTION: Identification of Essential Genes in *Staphylococcus aureus*, *ps*
; TITLE OF INVENTION: aeruginosa, klebsiella pneumoniae, salmonella typhimurium, an
; FILE REFERENCE: ELITRA.017PR5
; CURRENT APPLICATION NUMBER: US/60/269, 308
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 4774
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4438
; LENGTH: 1349
; TYPE: PR1
; ORGANISM: *Staphylococcus aureus*
US-60-269-308-4438

Query Match 3.7%; Score 147; DB 23; Length 1349;
Best Local Similarity 20.2%; Pred. No. 0.01;
Matches 203; Conservative 91; Mismatches 338; Indels 372; Gaps 44;

QY 8 NKLNTLTQRLVLSKNS--KRFYVTVGVFLMIFALVSMGCAKTVFGLVDSRP----- 59
Db 208 NSNNENNADIIIPKSTAPRLNTR-----MRIAIVGSSSTPAKAVNLDLITSNTLTLYVDA 262
QY 60 ---NAINP--DSSEYRWYGESEYRGHPYKQFRVAHDLRVNLGSRSEYQYCFNLKKA 114
Db 263 DKNKRIVPADYLSLKQIIVDDKVKSGDYF-----TIKSDYVQVYGLNPEDI 311
QY 115 FPLGS-----DSSVKKWKKHKG-----ISTKPEDYAMPRTITGDELNOKLRAVYNGH-- 163
Db 312 KNIDIDDPNNGETIATAKHDTANNLITTYFTDYV-----DFNVSVOGINKYSTYMDA 364
QY 164 ---PONANGIMELEPIANIRVTOEAVWYYSNAPISNPDESFRSEBSNL----- 211
Db 365 DTIVSKNDVEFNVTINTTAKTANIQIDPYVYVNEKNSIGSAPTEIVSHVGNKENPGY 424

